# STIC Biotechnology Systems Branch

# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/534,742 A_
Source: _Pur_
Date Processed by STIC: _3/20/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: *10/534,742A* |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 _____ Use of <220> — Sequence(s) *44* missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

RAW SEQUENCE LISTING                    DATE: 03/20/2006
PATENT APPLICATION:  US/10/534,742A     TIME: 12:27:37

Input Set : A:\10534742.txt
Output Set: N:\CRF4\03202006\J534742A.raw

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 3 <110> APPLICANT: Corrado FOGHER
 5 <120> TITLE OF INVENTION: Food flours with specific technological characteristics and
low
 6       allergenicity
 8 <130> FILE REFERENCE: 4161-12 / BX1898R
10 <140> CURRENT APPLICATION NUMBER: US 10/534,742A
11 <141> CURRENT FILING DATE: 2005-05-12
13 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/005092
14 <151> PRIOR FILING DATE: 2003-11-12
16 <150> PRIOR APPLICATION NUMBER: IT BO2002A000714
17 <151> PRIOR FILING DATE: 2002-11-13
19 <160> NUMBER OF SEQ ID NOS: 44
21 <170> SOFTWARE: MS Word
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 830
25 <212> TYPE: PRT
26 <213> ORGANISM: Wheat
28 <400> SEQUENCE: 1
30 Met Thr Lys Arg Leu Val Leu Phe Ala Ala Val Val Val Ala Leu Val
31 1               5                   10                  15
33 Ala Leu Thr Ala Ala Glu Gly Glu Ala Ser Gly Gln Leu Gln Cys Glu
34               20                  25                  30
36 Arg Glu Leu Gln Glu His Ser Leu Lys Ala Cys Arg Gln Val Val Asp
37           35                  40                  45
39 Gln Gln Leu Arg Asp Val Ser Pro Glu Cys Gln Pro Val Gly Gly Gly
40       50                  55                  60
42 Pro Val Ala Arg Gln Tyr Glu Gln Gln Val Val Val Pro Pro Lys Gly
43 65                  70                  75                  80
45 Gly Ser Phe Tyr Pro Gly Glu Thr Thr Pro Pro Gln Gln Leu Gln Gln
46               85                  90                  95
48 Ser Ile Leu Trp Gly Ile Pro Ala Leu Leu Arg Arg Tyr Tyr Leu Ser
49               100                 105                 110
51 Val Thr Ser Pro Gln Gln Val Ser Tyr Tyr Pro Gly Gln Ala Ser Ser
52           115                 120                 125
54 Gln Arg Pro Gly Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Glu Tyr
55       130                 135                 140
57 Tyr Leu Thr Ser Pro Gln Gln Ser Gly Gln Trp Gln Gln Pro Gly Gln
58 145                 150                 155                 160
60 Gly Gln Ala Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Glu
61               165                 170                 175
63 Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Trp Gln Pro Glu Gln Leu Gln
64               180                 185                 190
66 Gln Pro Thr Gln Gly Gln Gln Arg Gln Gln Pro Gly Gln Gly Gln Gln
67               195                 200                 205
```

**Does Not Comply**
**Corrected Diskette Needed**

```
69  Leu Arg Gln Gly Gln Gln Gly Gln Gln Ser Gly Gln Gly Gln Pro Arg
70      210             215             220
72  Tyr Tyr Pro Thr Ser Ser Gln Gln Pro Gly Gln Leu Gln Gln Leu Ala
73  225             230             235             240
75  Gln Gly Gln Gln Gly Gln Gln Pro Glu Arg Gly Gln Gln Gly Gln Gln
76              245             250             255
78  Ser Gly Gln Gly Gln Gln Leu Gly Gln Gly Gln Gln Gly Gln Gln Pro
79              260             265             270
81  Gly Gln Lys Gln Gln Ser Gly Gln Gly Gln Gln Gly Tyr Tyr Pro Ile
82          275             280             285
84  Ser Pro Gln Gln Leu Gly Gln Gly Gln Gln Ser Gly Gln Gly Gln Leu
85      290             295             300
87  Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly Gln Ser Gly
88  305             310             315             320
90  Tyr Tyr Pro Thr Ser Ala Gln Gln Pro Gly Gln Leu Gln Gln Ser Thr
91              325             330             335
93  Gln Glu Gln Gln Leu Gly Gln Glu Gln Gln Asp Gln Gln Ser Gly Gln
94              340             345             350
96  Gly Arg Gln Gly Gln Gln Ser Gly Gln Arg Gln Gln Asp Gln Gln Ser
97          355             360             365
99  Gly Gln Gly Gln Gln Pro Gly Gln Arg Gln Pro Gly Tyr Tyr Ser Thr
100     370             375             380
102 Ser Pro Gln Gln Leu Gly Gln Gly Gln Pro Arg Tyr Tyr Pro Thr Ser
103 385             390             395             400
105 Pro Gln Gln Pro Gly Gln Glu Gln Gln Pro Arg Gln Leu Gln Gln Pro
106             405             410             415
108 Glu Gln Gly Gln Gln Gly Gln Gln Pro Glu Gln Gly Gln Gln Gly Gln
109             420             425             430
111 Gln Pro Gly Gln Gly Glu Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln
112         435             440             445
114 Gly Gln Gln Pro Gly Gln Gly Gln Pro Gly Tyr Tyr Pro Thr Ser Pro
115     450             455             460
117 Gln Gln Ser Gly Gln Gly Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Gln
118 465             470             475             480
120 Gln Ser Gly Gln Leu Gln Gln Pro Ala Gln Gly Gln Gln Pro Gly Gln
121             485             490             495
123 Glu Gln Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Gly Gln Gln Pro
124             500             505             510
126 Gly Gln Gly Gln Gln Pro Gly Gln Gly Gln Pro Gly Tyr Tyr Pro Thr
127     515             520             525
129 Ser Pro Gln Gln Ser Gly Gln Glu Gln Gln Leu Glu Gln Trp Gln Gln
130     530             535             540
132 Ser Gly Gln Gly Gln Pro Gly His Tyr Pro Thr Ser Pro Leu Gln Pro
133 545             550             555             560
135 Gly Gln Gly Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ile Gly
136             565             570             575
138 Gln Gly Gln Gln Pro Gly Gln Leu Gln Gln Pro Thr Gln Gly Gln Gln
139         580             585             590
141 Gly Gln Gln Pro Gly Gln Gly Gln Gln Gly Gln Gln Pro Gly Gln Gly
```

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142         595                    600                     605
144 Gln Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Pro Gly Gln Gly Gln
145     610                   615                     620
147 Pro Gly Tyr Tyr Pro Thr Ser Leu Gln Gln Ser Gly Gln Gly Gln Gln
.148 625                   630               635                   640
150 Pro Gly Gln Trp Gln Gln Pro Gly Gln Gly Leu Pro Gly Tyr Tyr Pro
151                   645               650                   655
153 Thr Ser Ser Leu Gln Pro Glu Gln Gly Gln Gln Gly Tyr Tyr Pro Thr
154                   660               665                   670
156 Ser Gln Gln Gln Pro Gly Gln Gly Pro Gln Pro Gly Gln Trp Gln Gln
157         675                   680               685
159 Ser Gly Gln Gly Gln Gln Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser
160     690                   695               700
162 Gly Gln Gly Gln Gln Pro Gly Gln Trp Leu Gln Pro Gly Gln Trp Leu
163 705                   710               715                   720
165 Gln Ser Gly Tyr Tyr Leu Thr Ser Pro Gln Gln Leu Gly Gln Gly Gln
166                   725               730                   735
168 Gln Pro Arg Gln Trp Leu Gln Pro Arg Gln Gly Gln Gln Gly Tyr Tyr
169 ..         740             .   . ..  745           .: .. 750
171 Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly Gln Gln Leu Gly Gln Gly
172         755                   760               765
174 Gln Gln Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly Gln
175     770                   775               780
177 Gln Gly Tyr Asp Ser Pro Tyr His Val Ser Ala Glu His Gln Ala Ala
178 785                   790               795                   800
180 Ser Leu Lys Val Ala Lys Ala Gln Gln Leu Ala Ala Gln Leu Pro Ala
181                   805               810                   815
183 Met Cys Arg Leu Glu Gly Gly Asp Ala Leu Leu Ala Ser Gln
184         820                   825               830
187 <210> SEQ ID NO: 2
188 <211> LENGTH: 815
189 <212> TYPE: PRT
190 <213> ORGANISM: Wheat
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195 1             5                10                15
197 Ala Leu Thr Ala Ala Glu Gly Glu Ala Ser Gly Gln Leu Gln Cys Glu
198             20               25               30
200 Arg Glu Leu Gln Glu His Ser Leu Lys Ala Cys Arg Gln Val Val Asp
201         35               40               45
203 Gln Gln Leu Arg Asp Val Ser Pro Glu Cys Gln Pro Val Gly Gly Gly
204     50               55               60
206 Pro Val Ala Arg Gln Tyr Glu Gln Gln Val Val Val Pro Pro Lys Gly
207 65               70               75               80
209 Gly Ser Phe Tyr Pro Gly Glu Thr Thr Pro Pro Gln Gln Leu Gln Gln
210             85               90               95
212 Ser Ile Leu Trp Gly Ile Pro Ala Leu Leu Arg Arg Tyr Tyr Leu Ser
213             100               105               110
215 Val Thr Ser Pro Gln Gln Val Ser Tyr Tyr Pro Gly Gln Ala Ser Ser
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```
216           115                    120                  125
218 Gln Arg Pro Gly Gln Gly Gln Gln Glu Tyr Tyr Leu Thr Ser Pro Gln
219      130                    135                  140
221 Gln Ser Gly Gln Trp Gln Gln Pro Gly Gln Gly Gln Ser Gly Tyr Tyr
222 145              .  150                  155                  160
224 Pro Thr Ser Pro Gln Gln Ser Gly Gln Lys Gln Pro Gly Tyr Tyr Pro
225              165              170                  175
227 Thr Ser Pro Trp Gln Pro Glu Gln Leu Gln Gln Pro Thr Gln Gly Gln
228              180              185                  190
230 Gln Arg Gln Gln Pro Gly Gln Gly Gln Gln Leu Arg Gln Gly Gln Gln
231      195                    200                  205
233 Gly Gln Gln Ser Gly Gln Gly Gln Pro Arg Tyr Tyr Pro Thr Ser Ser
234      210                    215                  220
236 Gln Gln Pro Gly Gln Leu Gln Gln Leu Ala Gln Gly Gln Gln Gly Gln
237 225                230                  235                  240
239 Gln Pro Glu Arg Gly Gln Gln Gly Gln Gln Ser Gly Gln Gly Gln Gln
240              245                  250                  255
242 Leu Gly Gln Gly Gln Gln Gly Gln Gln Pro Gly Gln Lys Gln Gln Ser
243              260                  265                ..270
245 Gly Gln Gly Gln Gln Gly Tyr Tyr Pro Ile Ser Pro Gln Gln Leu Gly
246      275                    280                  285
248 Gln Gly Gln Gln Ser Gly Gln Gly Gln Leu Gly Tyr Tyr Pro Thr Ser
249      290                    295                  300
251 Pro Gln Gln Ser Gly Gln Gly Gln Ser Gly Tyr Tyr Pro Thr Ser Ala
252 305                310                  315                  320
254 Gln Gln Pro Gly Gln Leu Gln Gln Ser Thr Gln Glu Gln Gln Leu Gly
255              325                  330                  335 ·
257 Gln Glu Gln Gln Asp Gln Gln Ser Gly Gln Gly Arg Gln Gly Gln Gln
258              340                  345                  350
260 Ser Gly Gln Arg Gln Gln Asp Gln Gln Ser Gly Gln Gly Gln Gln Pro
261      355                    360                  365
263 Gly Gln Arg Gln Pro Gly Tyr Tyr Ser Thr Ser Pro Gln Gln Leu Gly
264      370                    375                  380
266 Gln Gly Gln Pro Arg Tyr Tyr Pro Thr Ser Pro Gln Gln Pro Gly Gln
267 385                390                  395                  400
269 Glu Gln Gln Pro Arg Gln Leu Gln Gln Pro Glu Gln Gly Gln Gln Gly
270              405                  410                  415
272 Gln Gln Pro Glu Gln Gly Gln Gln Gly Gln Gln Gln Arg Gln Gly Glu
273              420                  425                  430
275 Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Gly Gln Gln Pro Gly Gln
276      435                    440                  445
278 Gly Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly
279      450                    455                  460
281 Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Leu Gln
282 465                470                  475                  480
284 Gln Pro Ala Gln Gly Gln Gln Pro Gly Gln Glu Gln Gln Gly Gln Gln
285              485                  490                  495
287 Pro Gly Gln Gly Gln Gln Pro Gly Gln Gly Gln Pro Gly Tyr Tyr Pro
288              500                  505                  510
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Input Set : A:\10534742.txt
Output Set: N:\CRF4\03202006\J534742A.raw

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290 Thr Ser Pro Gln Gln Ser Gly Gln Glu Gln Gln Leu Glu Gln Trp Gln
291         515             520             525
293 Gln Ser Gly Gln Gly Gln Pro Gly His Tyr Pro Thr Ser Pro Leu Gln
294         530             535             540
296 Pro Gly Gln Gly Gln Pro Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ile
297 545             550             555             560
299 Gly Gln Gly Gln Gln Pro Gly Gln Leu Gln Gln Pro Thr Gln Gly Gln
300             565             570             575
302 Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Gly Gln Gln Pro Gly Glu
303         580             585             590
305 Gly Gln Gln Gly Gln Gln Pro Gly Gln Gly Gln Gln Pro Gly Gln Gly
306         595             600             605
308 Gln Pro Gly Tyr Tyr Pro Thr Ser Leu Gln Gln Ser Gly Gln Gly Gln
309         610             615             620
311 Gln Pro Gly Gln Trp Gln Gln Pro Gly Gln Gly Gln Pro Gly Tyr Tyr
312 625             630             635             640
314 Pro Thr Ser Ser Leu Gln Pro Glu Gln Gly Gln Gln Gly Tyr Tyr Pro
315             645             650             655
317 Thr Ser Gln Gln Gln Pro Gly Gln Gly Pro Gln Pro Gly Gln Trp Gln
318         660             665             670
320 Gln Ser Gly Gln Gly Gln Gln Gly Tyr Tyr Pro Thr Ser Pro Gln Gln
321         675             680             685
323 Ser Gly Gln Gly Gln Gln Pro Gly Gln Trp Leu Gln Pro Gly Gln Trp
324         690             695             700
326 Leu Gln Ser Gly Tyr Tyr Leu Thr Ser Pro Gln Gln Leu Gly Gln Gly
327 705             710             715             720
329 Gln Gln Pro Arg Gln Trp Leu Gln Pro Arg Gln Gly Gln Gln Gly Tyr
330             725             730             735
332 Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly Gln Gln Leu Gly Gln
333             740             745             750
335 Gly Gln Gln Gly Tyr Tyr Pro Thr Ser Pro Gln Gln Ser Gly Gln Gly
336             755             760             765
338 Gln Gln Gly Tyr Asp Ser Pro Tyr His Val Ser Ala Glu His Gln Ala
339         770             775             780
341 Ala Ser Leu Lys Val Ala Lys Ala Gln Gln Leu Ala Ala Gln Leu Pro
342 785             790             795             800
344 Ala Met Cys Arg Leu Glu Gly Gly Asp Ala Leu Leu Ala Ser Gln
345             805             810             815
347 <210> SEQ ID NO: 3
348 <211> LENGTH: 839
349 <212> TYPE: PRT
350 <213> ORGANISM: Wheat
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357 Ala Leu Thr Val Ala Glu Gly Glu Ala Ser Glu Gln Leu Gln Cys Glu
358             20              25              30
360 Arg Glu Leu Gln Glu Leu Gln Glu Arg Glu Leu Lys Ala Cys Gln Gln
361         35              40              45
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```
<210>  44
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Gln at position 4 may be mutated

<220>
<221>  misc_feature
<222>  (2)..(2)
<223>  Xaa can be any naturally occurring amino acid

<400>  44

Gln Xaa Pro Gln Gln Pro Gln Gln Phe
1               5
```

*(handwritten note)* needs explanation in ¿2207-¿2237 section (see item 11 on Error summary sheet)

**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:44; Xaa Pos. 2